



IFWO

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/10/625,202**

DATE: 08/31/2004  
 TIME: 15:07:15

Input Set : A:\89DIV.ST25.txt  
 Output Set: N:\CRF4\08312004\J625202.raw

3 <110> APPLICANT: Figdor, Carl Gustav  
 4 Geijtenbeek, Teunis Bernard Herman  
 5 Van Kooyk, Yvette  
 6 Torensma, Ruurd  
 8 <120> TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING DENDRITIC CELL-T CELL  
 9 INTERACTION  
 11 <130> FILE REFERENCE: 89 DIV  
 13 <140> CURRENT APPLICATION NUMBER: US 10/625,202  
 14 <141> CURRENT FILING DATE: 2003-07-23  
 16 <150> PRIOR APPLICATION NUMBER: 09/719,961  
 17 <151> PRIOR FILING DATE: 2001-09-24  
 19 <150> PRIOR APPLICATION NUMBER: PCT/NL00/00253  
 20 <151> PRIOR FILING DATE: 2000-04-19  
 22 <150> PRIOR APPLICATION NUMBER: US 60/176,924  
 23 <151> PRIOR FILING DATE: 2000-01-20  
 25 <150> PRIOR APPLICATION NUMBER: EP 99201204.7  
 26 <151> PRIOR FILING DATE: 1999-04-19  
 28 <160> NUMBER OF SEQ ID NOS: 2  
 30 <170> SOFTWARE: PatentIn version 3.2  
 32 <210> SEQ ID NO: 1  
 33 <211> LENGTH: 1215  
 34 <212> TYPE: DNA  
 35 <213> ORGANISM: Homo sapiens  
 38 <220> FEATURE:  
 39 <221> NAME/KEY: CDS  
 40 <222> LOCATION: (1)..(1215)  
 42 <400> SEQUENCE: 1  
  
 43 atg agt gac tcc aag gaa cca aga ctg cag ctg ggc ctc ctg gag 48  
 44 Met Ser Asp Ser Lys Glu Pro Arg Leu Gln Gln Leu Gly Leu Leu Glu  
 45 1 5 10 15  
 47 gag gaa cag ctg aga ggc ctt gga ttc cga cag act cga gga tac aag 96  
 48 Glu Glu Gln Leu Arg Gly Leu Gly Phe Arg Gln Thr Arg Gly Tyr Lys  
 49 20 25 30  
 51 agc tta gca ggg tgt ctt ggc cat ggt ccc ctg gtg ctg caa ctc ctc 144  
 52 Ser Leu Ala Gly Cys Leu Gly His Gly Pro Leu Val Leu Gln Leu Leu  
 53 35 40 45  
 55 tcc ttc acg ctc ttg gct ggg ctc ctt gtc caa gtg tcc aag gtc ccc 192  
 56 Ser Phe Thr Leu Ala Gly Leu Leu Val Gln Val Ser Lys Val Pro  
 57 50 55 60  
 59 agc tcc ata agt cag gaa caa tcc agg caa gac gcg atc tac cag aac 240  
 60 Ser Ser Ile Ser Gln Glu Gln Ser Arg Gln Asp Ala Ile Tyr Gln Asn  
 61 65 70 75 80  
 63 ctg acc cag ctt aaa gct gca gtg ggt gag ctc tca gag aaa tcc aag 288



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64	Leu	Thr	Gln	Leu	Lys	Ala	Ala	Val	Gly	Glu	Leu	Ser	Glu	Lys	Ser	Lys	
65				85					90					95			
67	ctg	cag	gag	atc	tac	cag	gag	ctg	acc	cag	ctg	aag	gct	gca	gtg	ggt	336
68	Leu	Gln	Glu	Ile	Tyr	Gln	Glu	Leu	Thr	Gln	Leu	Lys	Ala	Ala	Val	Gly	
69				100					105					110			
71	gag	ctt	cca	gag	aaa	tct	aag	ctg	cag	gag	atc	tac	cag	gag	ctg	acc	384
72	Glu	Leu	Pro	Glu	Lys	Ser	Lys	Leu	Gln	Glu	Ile	Tyr	Gln	Glu	Leu	Thr	
73				115					120					125			
75	cgg	ctg	aag	gct	gca	gtg	ggt	gag	ctt	cca	gag	aaa	tct	aag	ctg	cag	432
76	Arg	Leu	Lys	Ala	Ala	Val	Gly	Glu	Leu	Pro	Glu	Lys	Ser	Lys	Leu	Gln	
77				130					135					140			
79	gag	atc	tac	cag	gag	ctg	acc	tgg	ctg	aag	gct	gca	gtg	ggt	gag	ctt	480
80	Glu	Ile	Tyr	Gln	Glu	Leu	Thr	Trp	Leu	Lys	Ala	Ala	Val	Gly	Glu	Leu	
81	145				150					155					160		
83	cca	gag	aaa	tct	aag	atg	cag	gag	atc	tac	cag	gag	ctg	act	cgg	ctg	528
84	Pro	Glu	Lys	Ser	Lys	Met	Gln	Glu	Ile	Tyr	Gln	Glu	Leu	Thr	Arg	Leu	
85				165					170					175			
87	aag	gct	gca	gtg	ggt	gag	ctt	cca	gag	aaa	tct	aag	cag	cag	gag	atc	576
88	Lys	Ala	Ala	Val	Gly	Glu	Leu	Pro	Glu	Lys	Ser	Lys	Gln	Gln	Glu	Ile	
89				180					185					190			
91	tac	cag	gag	ctg	acc	cgg	ctg	aag	gct	gca	gtg	ggt	gag	ctt	cca	gag	624
92	Tyr	Gln	Glu	Leu	Thr	Arg	Leu	Lys	Ala	Ala	Val	Gly	Glu	Leu	Pro	Glu	
93				195					200					205			
95	aaa	tct	aag	cag	cag	gag	atc	tac	cag	gag	ctg	acc	cgg	ctg	aag	gct	672
96	Lys	Ser	Lys	Gln	Gln	Glu	Ile	Tyr	Gln	Glu	Leu	Thr	Arg	Leu	Lys	Ala	
97				210					215					220			
99	gca	gtg	ggt	gag	ctt	cca	gag	aaa	tct	aag	cag	cag	gag	atc			720
100	Ala	Val	Gly	Glu	Leu	Pro	Glu	Lys	Ser	Lys	Gln	Gln	Glu	Ile	Tyr	Gln	
101	225				230					235					240		
103	gag	ctg	acc	cag	ctg	aag	gct	gca	gtg	gaa	cgc	ctg	tgc	cac	ccc	tgt	768
104	Glu	Leu	Thr	Gln	Leu	Lys	Ala	Ala	Val	Glu	Arg	Leu	Cys	His	Pro	Cys	
105				245					250					255			
107	ccc	tgg	gaa	tgg	aca	ttc	tcc	caa	gga	aac	tgt	tac	ttc	atg	tct	aac	816
108	Pro	Trp	Glu	Trp	Thr	Phe	Phe	Gln	Gly	Asn	Cys	Tyr	Phe	Met	Ser	Asn	
109				260					265					270			
111	tcc	cag	cgg	aac	tgg	cac	gac	tcc	atc	acc	gcc	tgc	aaa	gaa	gtg	ggg	864
112	Ser	Gln	Arg	Asn	Trp	His	Asp	Ser	Ile	Thr	Ala	Cys	Lys	Glu	Val	Gly	
113				275					280					285			
115	gcc	cag	ctc	gtc	gta	atc	aaa	agt	gct	gag	gag	cag	aac	ttc	cta	cag	912
116	Ala	Gln	Leu	Val	Val	Ile	Lys	Ser	Ala	Glu	Glu	Gln	Asn	Phe	Leu	Gln	
117				290					295					300			
119	ctg	cag	tcc	aga	agt	aac	cgc	ttc	acc	tgg	atg	gga	ctt	tca	gat		960
120	Leu	Gln	Ser	Ser	Arg	Ser	Asn	Arg	Phe	Thr	Trp	Met	Gly	Leu	Ser	Asp	
121	305				310					315					320		
123	cta	aat	cag	gaa	ggc	acg	tgg	caa	tgg	gtg	gac	ggc	tca	cct	ctg	ttg	1008
124	Leu	Asn	Gln	Glu	Gly	Thr	Trp	Gln	Trp	Val	Asp	Gly	Ser	Pro	Leu	Leu	
125				325					330					335			
127	ccc	agg	tcc	aag	cag	tat	tgg	aac	aga	gga	gag	ccc	aac	aac	gtt	ggg	1056
128	Pro	Ser	Phe	Lys	Gln	Tyr	Trp	Asn	Arg	Gly	Glu	Pro	Asn	Asn	Val	Gly	

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129	340	345	350	
131	gag gaa gac tgc gcg gaa ttt agt ggc aat ggc tgg aac gac gac aaa			1104
132	Glu Glu Asp Cys Ala Glu Phe Ser Gly Asn Gly Trp Asn Asp Asp Lys			
133	355	360	365	
135	tgt aat ctt gcc aaa ttc tgg atc tgc aaa aag tcc gca gcc tcc tgc			1152
136	Cys Asn Leu Ala Lys Phe Trp Ile Cys Lys Ser Ala Ala Ser Cys			
137	370	375	380	
139	tcc agg gat gaa gaa cag ttt ctt tct cca gcc cct gcc acc cca aac			1200
140	Ser Arg Asp Glu Glu Gln Phe Leu Ser Pro Ala Pro Ala Thr Pro Asn			
141	385	390	395	400
143	ccc cct cct gcg tag			1215
144	Pro Pro Pro Ala			
148	<210> SEQ ID NO: 2			
149	<211> LENGTH: 404			
150	<212> TYPE: PRT			
151	<213> ORGANISM: Homo sapiens			
153	<400> SEQUENCE: 2			
155	Met Ser Asp Ser Lys Glu Pro Arg Leu Gln Gln Leu Gly Leu Leu Glu			
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159	Glu Glu Gln Leu Arg Gly Leu Gly Phe Arg Gln Thr Arg Gly Tyr Lys			
160	20	25	30	
163	Ser Leu Ala Gly Cys Leu Gly His Gly Pro Leu Val Leu Gln Leu Leu			
164	35	40	45	
167	Ser Phe Thr Leu Leu Ala Gly Leu Leu Val Gln Val Ser Lys Val Pro			
168	50	55	60	
171	Ser Ser Ile Ser Gln Glu Gln Ser Arg Gln Asp Ala Ile Tyr Gln Asn			
172	65	70	75	80
175	Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Ser Glu Lys Ser Lys			
176	85	90	95	
179	Leu Gln Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys Ala Ala Val Gly			
180	100	105	110	
183	Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr			
184	115	120	125	
187	Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln			
188	130	135	140	
191	Glu Ile Tyr Gln Glu Leu Thr Trp Leu Lys Ala Ala Val Gly Glu Leu			
192	145	150	155	160
195	Pro Glu Lys Ser Lys Met Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu			
196	165	170	175	
199	Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile			
200	180	185	190	
203	Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu			
204	195	200	205	
207	Lys Ser Lys Gln Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala			
208	210	215	220	
211	Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile Tyr Gln			
212	225	230	235	240
215	Glu Leu Thr Gln Leu Lys Ala Ala Val Glu Arg Leu Cys His Pro Cys			
216	245	250	255	

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219 Pro Trp Glu Trp Thr Phe Phe Gln Gly Asn Cys Tyr Phe Met Ser Asn  
220 260 265 270  
223 Ser Gln Arg Asn Trp His Asp Ser Ile Thr Ala Cys Lys Glu Val Gly  
224 275 280 285  
227 Ala Gln Leu Val Val Ile Lys Ser Ala Glu Glu Gln Asn Phe Leu Gln  
228 290 295 300  
231 Leu Gln Ser Ser Arg Ser Asn Arg Phe Thr Trp Met Gly Leu Ser Asp  
232 305 310 315 320  
235 Leu Asn Gln Glu Gly Thr Trp Gln Trp Val Asp Gly Ser Pro Leu Leu  
236 325 330 335  
239 Pro Ser Phe Lys Gln Tyr Trp Asn Arg Gly Glu Pro Asn Asn Val Gly  
240 340 345 350  
243 Glu Glu Asp Cys Ala Glu Phe Ser Gly Asn Gly Trp Asn Asp Asp Lys  
244 355 360 365  
247 Cys Asn Leu Ala Lys Phe Trp Ile Cys Lys Lys Ser Ala Ala Ser Cys  
248 370 375 380  
251 Ser Arg Asp Glu Glu Gln Phe Leu Ser Pro Ala Pro Ala Thr Pro Asn  
252 385 390 395 400  
255 Pro Pro Pro Ala

**VERIFICATION SUMMARY**

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